==========
Sequence Listing was accepted.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2009; month=3; day=17; hr=15; min=17; sec=57; ms=768;]
==========

Validated By CRFValidator v 1.0.3

Application No: 10549262 Version No: 2.0

Input Set:

Output Set:

Started: 2009-02-24 11:10:51.080
Finished: 2009-02-24 11:10:51.344
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 264 ms
Total Warnings: 0
Total Errors: 2
No. of SeqIDs Defined: 6
Actual SeqID Count: 6

Error code	Error Description
E 201	Mandatory field data missing in <140>
E 201	Mandatory field data missing in <141>

SEQUENCE LISTING

<110> Forschungszentrum Juelich GmbH

<120> Method for Microbial Production of L-Serine

<130> 23369

<140> 10549262
<141> 2006-05-10

<160> 6

<170> PatentIn Ver. 2.1

<210> 1
<211> 1449
<212> DNA
<213> Corynebacterium glutamicum

<400> 1
tcgtgcaact tcagactctt acggaggcga tggaccaaaa acaactacaa tcaagcagat 60
caccttgtac accaccatag aaaaggccca ccctcagcca tggctatcag tgttgttgat 120
ctatttagca tcggtatcgg accatcatcc tcacataccg tcggccccat gagagccgcc 180
ctcacgtata tctctgaatt tcccagctcg catgtcgata tcacgttgca cggatccctt 240
gccgccaccg gtaaaggcca ctgcactgac cgggcggtat tactgggtct ggtgggatgg 300
gaaccaacga tagttcccat tgatgctgca ccctcacccg gcgcgccgat tcctgcgaaa 360
ggttctgtga acgggccaaa gggaacggtg tcgtattccc tgacgtttga tcctcatcct 420
cttccagaac accccaatgc cgttaccttt aaaggatcaa ccacaaggac ttatttgtcg 480
gtgggtggtg ggttcattat gacgttggag gatttccgga agctggacga tatcggatca 540
ggtgtgtcaa ccattcatcc agaggcagag gtgccttgtc cttttcagaa gagttcccaa 600
ttactcgcat atggtcgcga ttttgcggag gtcatgaagg ataatgagcg cttaatccac 660
ggggatcttg gcacagtgga tgcccatttg gatcgagtgt ggcagattat gcaggagtgc 720
gtggcacaag gcatcgcaac gccggggatt ttaccgggtg ggttgaatgt gcaacgtcgg 780
gcgccgcagg tacacgcgct gattagcaac ggggatacgt gtgagctggg tgctgatctt 840
gatgctgtgg agtgggtgaa tctgtacgcc ttggcggtga atgaagaaaa cgccgctggt 900
ggtcgtgtgg ttactgctcc gactaatggt gctgcgggga ttattccggc ggtgatgcac 960
tatgcgcggg atttttgac aggttttggg gcggagcagg cgcggacgtt tttgtatacc 1020
gcgggtgcgg tgggcatcat cattaaggaa aatgcctcga tctctggcgc ggaggtgggg 1080
tgtcagggtg aggttggttc agcgtccgcg atggcggctg ccgggttgtg tgcagtctta 1140
ggtggttctc cgcaacaggt ggaaaacgcc gcggagattg cgttggagca caatttggga 1200
ttgacgtgcg atccggtggg cgggttagtg cagattccgt gtattgaacg caacgctatt 1260
gctgccatga agtccatcaa tgcggcaagg cttgcccgga ttggtgatgg caacaatcgc 1320
gtgagtttgg atgatgtggt ggtcacgatg gctgccaccg gccgggacat gctgaccaaa 1380
tataaggaaa cgtcccttgg tggtttggca accaccttgg gcttcccggt gtcgatgacg 1440
gagtgttag 1449

<210> 2
<211> 449
<212> PRT
<213> Corynebacterium glutamicum

<400> 2
Met Ala Ile Ser Val Val Asp Leu Phe Ser Ile Gly Ile Gly Pro Ser
1 5 10 15

```
Ser Ser His Thr Val Gly Pro Met Arg Ala Ala Leu Thr Tyr Ile Ser
             20                  25                  30

Glu Phe Pro Ser Ser His Val Asp Ile Thr Leu His Gly Ser Leu Ala
         35                  40                  45

Ala Thr Gly Lys Gly His Cys Thr Asp Arg Ala Val Leu Leu Gly Leu
     50                  55                  60

Val Gly Trp Glu Pro Thr Ile Val Pro Ile Asp Ala Ala Pro Ser Pro
 65                  70                  75                  80

Gly Ala Pro Ile Pro Ala Lys Gly Ser Val Asn Gly Pro Lys Gly Thr
                 85                  90                  95

Val Ser Tyr Ser Leu Thr Phe Asp Pro His Pro Leu Pro Glu His Pro
            100                 105                 110

Asn Ala Val Thr Phe Lys Gly Ser Thr Thr Arg Thr Tyr Leu Ser Val
        115                 120                 125

Gly Gly Gly Phe Ile Met Thr Leu Glu Asp Phe Arg Lys Leu Asp Asp
    130                 135                 140

Ile Gly Ser Gly Val Ser Thr Ile His Pro Glu Ala Glu Val Pro Cys
145                 150                 155                 160

Pro Phe Gln Lys Ser Ser Gln Leu Leu Ala Tyr Gly Arg Asp Phe Ala
                165                 170                 175

Glu Val Met Lys Asp Asn Glu Arg Leu Ile His Gly Asp Leu Gly Thr
            180                 185                 190

Val Asp Ala His Leu Asp Arg Val Trp Gln Ile Met Gln Glu Cys Val
        195                 200                 205

Ala Gln Gly Ile Ala Thr Pro Gly Ile Leu Pro Gly Gly Leu Asn Val
    210                 215                 220

Gln Arg Arg Ala Pro Gln Val His Ala Leu Ile Ser Asn Gly Asp Thr
225                 230                 235                 240

Cys Glu Leu Gly Ala Asp Leu Asp Ala Val Glu Trp Val Asn Leu Tyr
                245                 250                 255

Ala Leu Ala Val Asn Glu Glu Asn Ala Ala Gly Gly Arg Val Val Thr
            260                 265                 270

Ala Pro Thr Asn Gly Ala Ala Gly Ile Ile Pro Ala Val Met His Tyr
        275                 280                 285

Ala Arg Asp Phe Leu Thr Gly Phe Gly Ala Glu Gln Ala Arg Thr Phe
    290                 295                 300

Leu Tyr Thr Ala Gly Ala Val Gly Ile Ile Ile Lys Glu Asn Ala Ser
305                 310                 315                 320
```

```
Ile Ser Gly Ala Glu Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ser
                325                 330                 335

Ala Met Ala Ala Ala Gly Leu Cys Ala Val Leu Gly Gly Ser Pro Gln
            340                 345                 350

Gln Val Glu Asn Ala Ala Glu Ile Ala Leu Glu His Asn Leu Gly Leu
        355                 360                 365

Thr Cys Asp Pro Val Gly Gly Leu Val Gln Ile Pro Cys Ile Glu Arg
    370                 375                 380

Asn Ala Ile Ala Ala Met Lys Ser Ile Asn Ala Ala Arg Leu Ala Arg
385                 390                 395                 400

Ile Gly Asp Gly Asn Asn Arg Val Ser Leu Asp Asp Val Val Val Thr
                405                 410                 415

Met Ala Ala Thr Gly Arg Asp Met Leu Thr Lys Tyr Lys Glu Thr Ser
            420                 425                 430

Leu Gly Gly Leu Ala Thr Thr Leu Gly Phe Pro Val Ser Met Thr Glu
        435                 440                 445

Cys
```

<210> 3
<211> 18
<212> DNA
<213> Corynebacterium glutamicum

<400> 3
tcgtgcaact tcagactc 18

<210> 4
<211> 39
<212> DNA
<213> Corynebacterium glutamicum

<400> 4
cccatccact aaacttaaac acgtcataat gaacccacc 39

<210> 5
<211> 39
<212> DNA
<213> Corynebacterium glutamicum

<400> 5
tgtttaagtt tagtggatgg gccgactaat ggtgctgcg 39

<210> 6

<211> 18
<212> DNA
<213> Corynebacterium glutamicum

<400> 6
cgggaagccc aaggtggt 18